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Preliminary estimation of longevity for leopard and snow leopard populations

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Abstract: *Preliminary estimation of longevity for leopard and snow leopard populations.* Longevity is the main functional trait, very important in the conservation and restitution breeding programs. This trait is determined by both genetic and environmental effects. The objective of this study was to estimate genetic variance of longevity in leopard and snow leopard populations kept in the zoological gardens. The data were extracted from the International Species Information System (ISIS). The analysis included pedigree information of 1434 and 1256 individuals born in 1915–2003 years (respectively for snow leopard and leopard). The estimation of genetic variance was performed by the Animal Model, using the derivative-free restricted maximum likelihood algorithm. Decreasing genetic variance has been noticed over time in the both populations. It may affect the lifespan and survival in the analyzed populations. Results of this paper suggest that reasonable breeding programs should aid to increasing the genetic variability.

Key words: captive population, genetic variance, Animal Model.

INTRODUCTION

Reduction of the genetic variability is one of the most important threats limiting conservation breeding (Princee, 1998). Occurrence of the high genetic variability is immeasurably advantageous for the process of reintroduction species. Because of the genetic disparity in the species, under environmental pressure individuals with high adaptation ability will be preferred (Crnokrak and Roff, 1999). Natural selection and mating in zoological gardens prefer generally genotypes easily adapted to peculiar environmental conditions. Although, knowledge of genetic variability is the one of the important elements, which can be used to evaluate usefulness of populations maintained in the controlled conditions for future reintroduction procedures (Sternicki, 2002).

Stabilization of genetic variability is one of the most important element for reintroduction of individuals, kept in zoological gardens under conservation of their gene pool procedures. For that reason, monitoring of genetic variability becomes a key element in populations. The aim of this paper was to estimate the genetic variance of longevity for leopard *Panthera pardus* and snow leopard *Uncia uncia*.

MATERIAL AND METHODS

The data were extracted from the ISIS (*International Species Information System*) data base. This base contain information about each individual in population (studbook number, birth and death date, number of sire and dam, transfers, etc.). Data set consisted records of 2080 snow leopards and 2452 leopards. Individuals of unknown death date were eliminated and in result 1434 and 1256 animals left, for snow leopard and leopard respectively. Table 1 presents the size of data and distribution of sexes within analyzed species.

TABLE 2. Average life length for analyzed data sets (in days)

Data	Number of individuals	Average life length (in days)	Standard Deviation
Panthera1	1 434	1 739	2 467.53
Panthera31	825	3 019	2 592.55
Uncia1	1 256	1 929	2 420.66
Uncia31	757	3 197	2 382.52

Panthera1, Uncia1 – all individuals, Panthera31, Uncia31 – individuals up to 31th day of life.

level of standard deviations of average lifespan in the analyzed group was caused by postnatal fatality and animals with long lifespan.

TABLE 1. Number of animals according to species and sex

Species	Number of individuals	Number of		
		males	females	individuals with unknown sex
Panthera pardus	1434	563	619	252
Uncia uncia	1256	560	551	145

Because of the high postnatal mortality, the data set was divided into two subclasses: all individuals (Panthera1, Uncia1) and animals up to 31th day of the lifetime (Panthera31, Uncia31). Table 2 presents the average lifespan in the subsets, according to species and class of longevity.

The data set included long period (1915–2003), and number of records in particular years were relatively small, so random additive predicts were used in the genetic variance, defined as an average predictors in 3 year subperiods. High

The genetic variance was estimated based on the Derivative Free Restricted Maximum Likelihood approach (DFREML) introduced by Smith and Graser (1986), numerically implemented by Meyer (1989).

An assumption of the animal model was used to construct the linear model of lifespan (Henderson, 1988). Known genetic and none-genetic factors were considered. Results of multivariate analysis of variation were used for creation of model because significant factors influenced into longevity were included as

fixed effects. There were: sex, birth date, place of birth, number of transfers, numbers of subspecies (in case of leopard) inbreeding coefficient (as covariable) and random additive genetic effect of individual. The coefficient of inbred (estimated using additive relationship matrix according to Henderson (1988)) was included into partial linear regression.

The following linear model was applied:

$$y_{ijkmno} = \mu + s_i + p_j + g_k + t_m + m_n + \\ + bx_{ijkmno} + a_{ijkmno} + e_{ijkmno}$$

where:

y_{ijkmno} – length of life (days) of ijkmno-th individual,
μ – overall mean,
s_i – the fixed effect of i-th sex,
p_j – the fixed effect of j-th period of birth,
g_k – the fixed effect of k-th subspecies group (for Leopard),
t_m – the fixed effect of t-th numbers of transfer,
m_n – the fixed effect of n-th place of birth (country),
b – linear regression coefficient,
y_{ijkmno} – the inbreeding coefficient of ijklmno-th individual (included as a covariable),
a_{ijkmno} – random additive genetic effect of ijkmno-th individual,
e_{ijkmno} – random error of ijkmno-th observation,

An assessment of the model accuracy was made on the basis of error variance value. Predictors of genetic effects, obtained from individuals grouped in three birth years periods, was estimated based on above-mentioned algorithm.

RESULTS AND DISCUSSION

Generally, changes of genetic variance level within analyzed data sets shown, that the shape of curves for both species is approximately similar. On Figure 1 fluctuation of longevity average

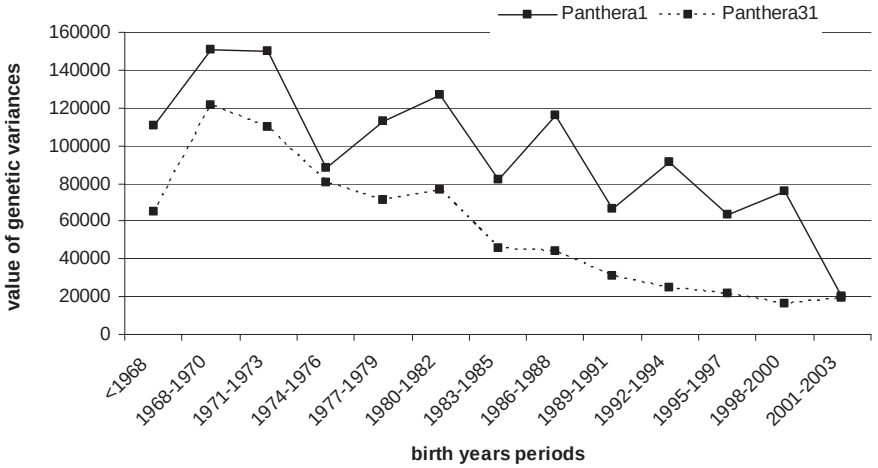

FIGURE 1. Fluctuation of genetic variance for leopard population

genetic variances in leopard population was shown. Curves of genetic variances depict a negative tendency. Larger values were noticed for all leopards (Panthera1), lower – for group which included the youngest animals with lifespan shorter than 31 day (Panthera31). Gradual decrease of genetic variances in time within every analyzed group was also observed.

The higher values with large fluctuation were noticed for all leopard (Panthera1), compared to the individuals that lead to the reduction of genetic variability. No doubt, this was caused by no or smaller addition of new not related animals. However, transfer of some individuals between zoos in last period was not recorded, which contribute to new unknown breeding lines and gave small fluctuation of genetic variance of lifespan in the years.

Similar course, with decreasing of genetic variance in time, was observed for snow leopard (Fig. 2). Higher genetic variance, in the leopard population than

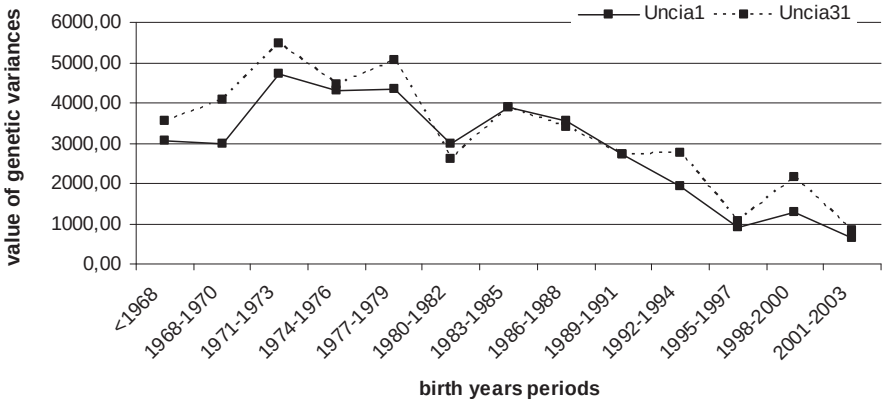

FIGURE 2. Fluctuation of genetic variance for snow leopard population

survived more than 31 days. Probably the large number of animals was the reason for slope change of the above-mentioned value. The high values of genetic variances in the first period of time (since 1970) were obtained due integration of new individuals from the wildlife. Probably, decrease of genetic variability after 1970 was caused by limited selection due to many relatives in population and snow leopard, could be observed from disparity of researched variability trait, because of coexistence several subspecies in the same data base.

An increase of genetic variance was observed in snow leopard population in first few years (since 1971). After that period, gradual decrease followed. Maximum fluctuation was shown in 1980–1985 with simultaneous insignif-

icant incrementation in 1996–2001. Big disparities in analyzed data for species were not noticed. Similar course of curve (insignificant change in scale) characterized animals from data set Uncia1, as well as Uncia31. Individuals survived more than 31 days are characterized by the highest value of genetic variance.

For both populations, during the analyzed period, it have been noticed a decrease of genetic variability. Both researched species are protected with international regulations (IUCN – The World Conservation Union and CITES – Convention on International Trade in Endangered Species of Wild Fauna and Flora) with prohibition of capturing the animals from their natural environments since 1975. In consequence of this low population maintained in the zoological garden, as small closed populations, are affected by increase level of homozygosity.

Incessant decrease of genetic variability seems to be a serious barrier in furthest breeding of the analyzed species due to erosion of gene pool which appears in populations kept in captivity for many years (Lacy, 1994).

From the point of view of conservation breeding, adverse individuals appear in population, because of decrease of adaptation (Lacy, 1993; Laurence and Smart, 2000) and also increase mortality (Crnokrak and Roff, 1999). In view of genetic variability reduction in analyzed populations in result is possible smaller capability of effective selection. This can contribute to future breeding. Comparing studies carried over other species, leads to the conclusion, that loosing of genetic variability and increase of inbreeding makes many difficulties for reintroduction programs (Thomas, 1987: Lacy, 1993; Laikre et al., 1996; Frankham, 1997; Olech, 2003). Moreover, negative result of increase of animal's homozygosity and decrease of genetic variability were shown in many small population of mammals kept in captivity (Ryan, 2003). Taking into account animals from zoological gardens under assumptions that environmental conditions are rather stable, the decrease of genetic variance is influenced by inbreeding increase. However, in the populations in which from the long period are relative mating, the increase of population size is often achieved at the cost of genetic variability (Wright, 1920). It may seem, that individuals from zoological gardens are not suitable for reintroduction because their adapting ability to natural biotopes may been lost. Decrease of genetic variances (with environmental effects) influenced deterioration of survival traits (Lacy, 1993). Because of this fact, population of endangered species, which are kept in zoological gardens, maintained a main species gene pool. In case of genetic variability decrease in analyzed populations of leopard and snow leopard with decrease of population size, the future breeding situation seems to be difficult.

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Streszczenie *Wstępne oszacowania długości życia populacji lamparta oraz śnieżnej pantery*. Długość życia jest bardzo ważną cechą dla ochrony gatunków oraz programów hodowlanych i restytucyjnych. Determinują ją zarówno czynniki genetyczne, jak i środowiskowe. Celem tych badań było oszacowanie wariancji genetycznej długości życia dla dwóch populacji kotowatych lamparta oraz śnieżnej pantery, utrzymywanych w warunkach ogrodu zoologicznego. Materiał badawczy stanowiły rodowody zwierząt skatalogowane w Międzynarodowym Systemie Informacji o Gatunkach (ISIS). Baza danych zawierała informacje o 1434 oraz 1256 (odpowiednio dla śnieżnej pantery oraz lamparta) osobnikach. Szacowania wariancji genetycznej dokonano przy pomocy Modelu Zwierzęcia (Animal Model), stosując algorytm klasycznej estymacji punktowej, największej wiarygodności z ograniczeniem. Zaobserwowano zmniejszający się w czasie poziom wariancji genetycznej w obu populacjach. Może mieć to wpływ na przeżywalność analizowanych populacji. Wyniki tej pracy sugerują konieczność prowadzenia programów hodowlanych w taki sposób, aby zwiększać wariancję genetyczną badanej cechy.

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